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	Type	L #	Hits	Search Text	DBs	Time Stamp	Comments	Error Definition	Errors
1	IS&R	L1	2178	(382/159,165,181,209,218,219,224,228).CCLS.	USPAT	2005/02/18 08:36			
2	BRS	L2	1872	structured same (similar\$5 or match\$3) same (differ\$5 or dissimilar\$5 or mismatch\$3 or unmatched\$3)	USPAT	2005/02/18 08:40			
3	BRS	L3	206	2 same (compar\$6 or correlat\$5 or collat\$3)	USPAT	2005/02/18 08:38			
4	BRS	L4	16	3 same (template\$1 or model\$1)	USPAT	2005/02/18 08:39			
5	BRS	L5	223186	(similar\$5 or match\$3) with (differ\$5 or dissimilar\$5 or mismatch\$3 or unmatched\$3)	USPAT	2005/02/18 08:42			
6	BRS	L6	3622	5 same vector\$1	USPAT	2005/02/18 08:40			
7	BRS	L7	728	6 same compar\$6	USPAT	2005/02/18 08:40			
8	BRS	L8	56	7 same model	USPAT	2005/02/18 08:41			
9	BRS	L9	10	8 same (sequence\$1 or tree or structured)	USPAT	2005/02/18 08:41			
10	BRS	L10	1	1 and 9	USPAT	2005/02/18 08:41			

	Type	L #	Hits	Search Text	DBs	Time Stamp	Comments	Error Definition	Errors
11	BRS	L11	338	(structured near3 (data or object\$1)) same model\$1	USPAT	2005/02/1 8 08:42			
12	BRS	L12	41	11 same (similar\$5 or match\$3)	USPAT	2005/02/1 8 08:42			
13	BRS	L13	9	12 same (differ\$5 or dissimilar\$5 or mismatch\$3 or unmatch\$3)	USPAT	2005/02/1 8 08:42			
14	BRS	L14	1	1 and 9	USPAT	2005/02/1 8 08:43			
15	BRS	L15	46288	(biopolymer or protein) same sequence\$1	USPAT	2005/02/1 8 08:44			
16	BRS	L16	41	2 and 15	USPAT	2005/02/1 8 08:44			

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Terms	Documents
L13 same (differ\$5 or mismatch\$3 or unmatched\$3 or dissimilar\$5)	14

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<u>L1</u>	(similarit\$3 or match\$3) same (differ\$5 or mismatch\$3 or unmatched\$3 or dissimilar\$5) same (template or model)	5878	<u>L1</u>
<u>L2</u>	L1 same compar\$6	1508	<u>L2</u>
<u>L3</u>	L2 same vector	156	<u>L3</u>
<u>L4</u>	L3 and (structured near2 (data or object or signal or image))	3	<u>L4</u>
<u>L5</u>	(biopolymer or protein) same sequence same model	5504	<u>L5</u>
<u>L6</u>	l5 same (differ\$5 or mismatch\$3 or unmatched\$3 or dissimilar\$5)	847	<u>L6</u>
<u>L7</u>	l6 same (differ\$5 or mismatch\$3 or unmatched\$3 or dissimilar\$5)	847	<u>L7</u>
<u>L8</u>	L7 same (model or template)	847	<u>L8</u>
<u>L9</u>	L8 same compar\$6	277	<u>L9</u>
<u>L10</u>	L9 same vector	58	<u>L10</u>
<u>L11</u>	structured data	1683	<u>L11</u>
<u>L12</u>	l1 same L11	2	<u>L12</u>

L13 l11 same model

101 L13

L14 l13 same (differ\$5 or mismatch\$3 or unmatched\$3 or dissimilar\$5)

14 L14

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((biopolymer* or protein*) <near/10> sequence*) <para

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1 Genomics and proteomics: a signal processor's tour

Vaidyanathan, P.P.;

Circuits and Systems Magazine, IEEE , Volume: 4 , Issue: 4 , Fourth Quarter :
Pages:6 - 29

[\[Abstract\]](#) [\[PDF Full-Text \(2994 KB\)\]](#) **IEEE JNL**

2 A Polynomial-Time Algorithm for the Matching of Crossing Contact-Map Patterns

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1 , Issue: 4 , Oct.-Dec. 2004
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3 Bio-Basis Function Neural Network for Prediction of Protease Cleavage Sites in Proteins

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Pages:263 - 274

[Abstract] [PDF Full-Text (600 KB)] IEEE JNL

4 Computational challenges of systems biology

Finkelstein, A.; Hetherington, J.; Linzhong Li; Margoninski, O.; Saffrey, P.; Seymour, R.; Warner, A.

Computer , Volume: 37 , Issue: 5 , May 2004

Pages:26 - 33

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5 **Genomewide motif identification using a dictionary model**

Sabatti, C.; Lange, K.;

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[\[Abstract\]](#) [\[PDF Full-Text \(403 KB\)\]](#) [\[Full-Text HTML\]](#) [IEEE JNL](#)

6 **Characterization of protein secondary structure**

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7 **Information geometric similarity measurement for near-random stochastic processes**

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Systems, Man and Cybernetics, Part A, IEEE Transactions on , Volume: 33 , Issue: 4 , July 2003

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8 **Investigation of the applicability of dielectric relaxation properties of amino acid solutions within the resonant recognition model**

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9 **Zippping out relevant information**

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10 **Automatic pattern embedding in protein structure models**

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11 **Integrated access to heterogeneous data from NCBI**

Ostell, J.M.;

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12 Dynamic, object-oriented parallel processing

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13 K-group A* for multiple sequence alignment with quasi-natural gap costs

Rong Zhou; Hansen, E.A.;

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14 A New Scheme for Protein Sequence Motif Extraction

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15 Recurrence time statistics: versatile tools for genomic DNA sequence analysis

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